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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/503,089

DATE: 03/03/2000

TIME: 11:28:35

Input Set: I503089.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

E--> 1 <110> PATEL, AMANDA J.
2 HONORE, ERIC
3 LESAGE, FLORIAN
4 ROMEY, GEORGES
5 LAZDUSKI, MICHEL
6 <120> A method for the identification of anesthetics
7 <130> f17b12prov3-humanTREK
8 <140> US/09/503,089
9 <141> 2000-02-11
10 <160> 4 (see last page)
11 <170> Wordperfect 8.0

ERRORED SEQUENCES FOLLOW

E--> 12 <210> 1
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14 <212> ADN DNA
15 <213> Homo sapiens
16 <220>
17 <221> CDS
18 <222> (1) .. (1236)
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22 1 5 10 15
23 aaa ccg agg ctc tcg ttt tcc acg aaa ccc aca gtg ctt gct tcc cgg 96
24 Lys Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg
25 20 25 30
26 gtg gag agt gac acg acc att aat gtt atg aaa tgg aag acg gtc tcc 144
27 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser
28 35 40 45
29 acg ata ttc ctg gtg gtt gtc ctc tat ctg atc atc gga gcc acc gtg 192
30 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
31 50 55 60
32 ttc aaa gca ttg gag cag cct cat gag att tca cag agg acc acc att 240
33 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile
34 65 70 75 80
35 gtg atc cag aag caa aca ttc ata tcc caa cat tcc tgt gtc aat tcg 288
36 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser
37 85 90 95
38 acg gag ctg gat gaa ctc att cag caa ata gtg gca gca ata aat gca 336
39 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala

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40			100			105			110								
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42	Gly	Ile	Ile	Pro	Leu	Gly	Asn	Thr	Ser	Asn	Gln	Ile	Ser	His	Trp	Asp	
43			115					120					125				
44	ttg	gga	agt	tcc	ttc	ttc	ttt	gct	ggc	act	gtt	att	aca	acc	ata	gga	432
45	Leu	Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	
46			130					135					140				
47	ttt	gga	aac	atc	tca	cca	cgc	aca	gaa	ggc	ggc	aaa	ata	ttc	tgt	atc	480
48	Phe	Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	
49			145				150					155			160		
50	atc	tat	gcc	tta	ctg	gga	att	ccc	ctc	ttt	ggg	ttt	ctc	ttg	gct	gga	528
51	Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	Gly	
52				165				170					175				
53	gtt	gga	gat	cag	cta	ggc	acc	ata	ttt	gga	aaa	gga	att	gcc	aaa	gtg	576
54	Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val	
55			180					185					190				
56	gaa	gat	acg	ttt	att	aag	tgg	aat	gtt	agt	cag	acc	aag	att	cgc	atc	624
57	Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile	
58			195					200					205				
59	atc	tca	aca	atc	ata	ttt	ata	cta	ttt	ggc	tgt	gta	ctc	ttt	gtg	gct	672
60	Ile	Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	Ala	
61			210				215					220					
62	ctg	cct	gcg	atc	ata	ttc	aaa	cac	ata	gaa	ggc	tgg	agt	gcc	ctg	gac	720
63	Leu	Pro	Ala	Ile	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	Asp	
64			225				230					235			240		
65	gcc	att	tat	ttt	gtg	gtt	atc	act	cta	aca	act	att	gga	ttt	ggg	gac	768
66	Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	
67				245				250					255				
68	tac	gtt	gca	ggg	gga	tcc	gat	att	gaa	tat	ctg	gac	ttc	tat	aag	cct	816
69	Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	Pro	
70			260					265					270				
71	gtc	gtg	tgg	ttc	tgg	atc	ctt	gta	ggg	ctt	gct	tac	ttt	gct	gct	gtc	864
72	Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	Val	
73			275					280					285				
74	ctg	agc	atg	att	gga	gat	tgg	ctc	cga	gtg	ata	tct	aaa	aag	aca	aaa	912
75	Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	Lys	
76			290				295					300					
77	gaa	gag	gtg	gga	gag	ttc	aga	gca	cac	gct	gct	gag	tgg	aca	gcc	aac	960
78	Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	Asn	
79			305				310					315			320		
80	gtc	aca	gcc	gaa	ttc	aaa	gaa	acc	agg	agg	cga	ctg	agt	gtg	gag	att	1008
81	Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	Ile	
82				325				330					335				
83	tat	gac	aag	ttc	cag	cgg	gcc	acc	tcc	atc	aag	cgg	aag	ctc	tcg	gca	1056
84	Tyr	Asp	Lys	Phe	Gln	Arg	Ala	Thr	Ser	Ile	Lys	Arg	Lys	Leu	Ser	Ala	
85			340					345					350				
86	gaa	ctg	gct	gga	aac	cac	aat	cag	gag	ctg	act	cct	tgt	agg	agg	acc	1104
87	Glu	Leu	Ala	Gly	Asn	His	Asn	Gln	Glu	Leu	Thr	Pro	Cys	Arg	Arg	Thr	
88			355					360					365				
89	ctg	tca	gtg	aac	cac	ctg	acc	aac	gag	agg	gat	gtc	ttg	cct	ccc	tta	1152

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92	ctg aag act gag agt atc tat ctg aat ggt ttg acg cca cac tgt gct	1200
93	Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala	
94	385 390 395 400	
95	ggt gaa gag att gct gtg att gag aac atc aaa tag	1236
96	Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys	
97	405 410	

E-->

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108	gaagaggggc tgcagtgatc accccctcgc tgagccccgg ggccagagccc agccgcccggc	180
109	cgagcgcacg gagccacggg ccgagcgcac ccagggcccc cgccgggaccc caggcggcca	240
110	cgcaatcggg gtgacctatc gcgcgggggg gcgtcgtcgt ccgatcccaa cttggcctcg	300
111	gcctcgcctt ctgcccagcc tgccaccgct ggtgtcctct ccttcggcg atttcgtttc	360
112	ttctcacgct cccccctcta taccctccc gcctccagcc ccgctctccc caccttgtaa	420
113	aacaaagccg gggaaaatgc ctaccctgtc agctcggagc gcgcagcccc tcttgggaata	480
114	agg atg gcg gcc cct gac ttg ctg gat ccc aag tct gct gct cag aac	528
115	Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn	
116	1 5 10 15	
117	tcc aaa ccg agg ctc tca ttc tcc tca aaa ccc acc gtg ctt gct tcc	576
118	Ser Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser	
119	20 25 30	
120	cgg gtg gag agt gac tcg gcc att aat gtt atg aaa tgg aag aca gtc	624
121	Arg Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val	
122	35 40 45	
123	tcc acg att ttc ctg gtg gtc gtc ctc tac ctg atc atc gga gcc gcg	672
124	Ser Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala	
125	50 55 60	
126	gtg ttc aag gca ttg gag cag cct cag gag att tcc cag agg acc acc	720
127	Val Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr	
128	65 70 75	
129	att gtg atc cag aag cag acc ttc ata gcc cag cat gcc tgc gtc aac	768
130	Ile Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn	
131	80 85 90 95	
132	tcc acc gag ctg gac gaa ctc atc cag caa ata gtg gca gca ata aac	816
133	Ser Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn	
134	100 105 110	
135	gca ggg att atc ccc tta gga aac agc tcc aat caa gtt agt cac tgg	864
136	Ala Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp	
137	115 120 125	
138	gac ctc gga agc tct ttc ttc ttt gct ggt act gtt atc aca acc ata	912

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192	gaagagtctg aggtggagcc ataggaaggg gcttctctag gctctttgtg actggtgccc	1789
193	gtagcattta aacattgtgc atggtgacct caaagggaaa gcaaatagaa aacacccatc	1849
194	tggtcacctt acatccaggg aggggtgtgt cccgaggcgg cactctgagg atgccgtgtg	1909
195	ctgtccgctg agtgctgagt gatggacagg cagtgtctga tgccttttgt gccagactg	1969
196	tttccctccc ccctctctcc taacgtgcca taaggcctat gaatgaatct gaatgctttg	2029
197	ctggtcatgt agattggagg gatcagccct tggtttttca tggttcacct aactgagcct	2089
198	ggatactgac cacttaggga tgacaacatt tctttttgta aatggcgaga aattcttacg	2149
199	cagcctttta cctaagaaat tttctgccag tgccttatct tatgaagaaa caagaccctg	2209
200	tctgggtggc ttgtggttcc tcccttcccc gccctcacgg tgggctcacc ctttgetgac	2269
201	tctcacctat cccctccccct ccgcatacct tattgtgctg gaagcaatgt gtggcttgat	2329
202	ggaagaaaca gatgccaact gcaggcacag aagcaacatg gaagctctgg cgtcacgggc	2389
203	actgcagaga agggaggtca gagaaggccc ctctgagtat ttatttgacc ggggtaccaa	2449
204	tggtagcgt atatatatgt acagagtaat aattcccagg ccggtaacct tggctgcttc	2509
205	cacacggccc ctttttttcc ctggcagtat ttgaagtta tcatttatta ataactagtc	2569
206	atttttaaaag gcagaagaag acatgagcac atacatctgt aatctacgtg atgtgataag	2629
207	aaaactgttc agactggtat tgcaagggtga tctcagacag tcgatatgga ttcattctga	2689
208	tgagaagaaa acagcgagac cacgtgtcgt gcgcagtagc tcatacaggg ctcactgtca	2749
209	gcttggaacca gcccgtagg tacagcaggc ttacacactt tcttttctta agtggttctt	2809
210	gccaaactgg agggaggggc gatgcccttc agaagggggc acagccccag ccagcccagg	2869
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212	tttgacatg gagagataca gactgctggc ataggtcgtc tctaacagta gagaaaacgc	2989
213	cgattagcac aatctaaatc ccccgagtag ctttttgttt aggataagag aaggctggta	3049
214	attcacttaa tttaaattta tatectataa ttctttttgg atgtttcaag attcagaaaa	3109
215	agtccagtcc ctgcatctag caaacgcgcg ccttttctc tgtgcccgtta cttacatcta	3169
216	ctgaacactg tatatgtaat ttttaaattt ttaaagcgca gaaggaaaat gattcttcta	3229
217	catgtaatcg caaaactgat ttctcccttc tgggggagggc ttgggcttac gtgatcatgt	3289
218	ggcattcaga gtaaagtctt aagacataaa cccaggatgt ttaaaaaacac aaaaagattc	3349
219	ctattttcca aaatttgaat ttaagctata aatgtaaata tatccagttc gcttgagag	3409
220	agtactttta taaacctatg aagattctaa ccaaaatttt aaaatgtcgg gttcctttac	3469
221	aaagaaagct ccacccatct cctgaatagc cgttttggaa gctgacatgg tgggatgtac	3529
222	cacgtataaa ctgtgaactg gaggacaaat aaagtgtgta attaaaaaaaa a	3580

See next page

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<211> 394

<212> PRT

<213> Mus sp.

<223> TASK

<400> 5

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 Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu
 35 40 45
 Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
 50 55 60
 Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
 65 70 75 80
 Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
 85 90 95
 Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
 100 105 110
 Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
 115 120 125
 Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
 130 135 140
 Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val
 145 150 155 160
 Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala
 165 170 175
 Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr
 180 185 190
 Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu
 195 200 205
 Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser
 210 215 220
 Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn
 225 230 235 240
 Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg
 245 250 255
 Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly Gly
 260 265 270
 Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr
 275 280 285
 Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu
 290 295 300
 His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys
 305 310 315 320
 Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser
 325 330 335
 Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly Arg
 340 345 350
 Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg
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 Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr Phe
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 Arg Gly Leu Met Lys Arg Arg Ser Ser Val
 385 390

*last sequence in file**>22207 <- insert this numeric identifier, series**22237 is shown*

Please review the
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 <223> fields of each sequence which presents at least one n or Xaa.

PVI